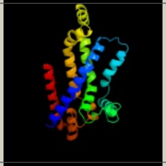
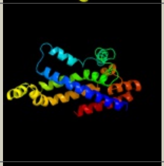
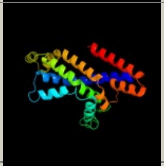
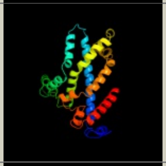
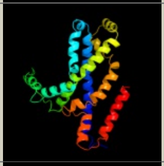
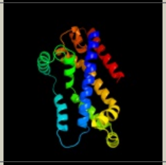
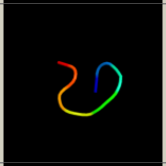
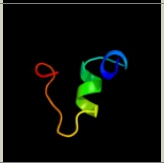
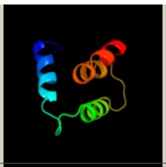
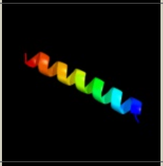
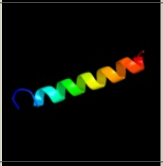
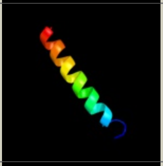
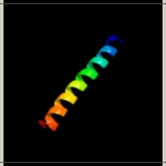
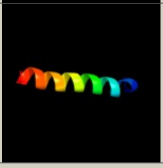
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0AFU0
Date	Thu Jan 5 11:27:15 GMT 2012
Unique Job ID	fcbe8746d9743e8d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3dhwa1	Alignment		99.9	19	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
2	d2onkc1	Alignment		99.8	17	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
3	c2onkC_	Alignment		99.8	17	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**molybdate/tungstate abc transporter, permease **PDBTitle:** abc transporter modbc in complex with its binding protein2 moda
4	d3d31c1	Alignment		99.8	16	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
5	c3d31D_	Alignment		99.8	16	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**sulfate/molybdate abc transporter, permease **PDBTitle:** modbc from methanosarcina acetivorans
6	d2r6gf2	Alignment		99.7	14	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
7	c2r6gF_	Alignment		99.6	14	**PDB header:**hydrolase/transport protein **Chain:** F: **PDB Molecule:**maltose transport system permease protein malf; **PDBTitle:** the crystal structure of the e. coli maltose transporter
8	c3fh6F_	Alignment		99.5	15	**PDB header:**transport protein **Chain:** F: **PDB Molecule:**maltose transport system permease protein malf; **PDBTitle:** crystal structure of the resting state maltose transporter from e.2 coli
9	d2r6gg1	Alignment		99.1	14	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
10	c1wz4A_	Alignment		21.8	50	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**major surface antigen; **PDBTitle:** solution conformation of adr subtype hbv pre-s2 epitope
11	c2cw1A_	Alignment		18.4	41	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**sn4m; **PDBTitle:** solution structure of the de novo-designed lambda cro fold2 protein

12	c1ciiA_	Alignment		16.1	11	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
13	c1y66D_	Alignment		13.6	21	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**engrailed homeodomain; **PDBTitle:** dioxane contributes to the altered conformation and2 oligomerization state of a designed engrailed homeodomain3 variant
14	c2ka1A_	Alignment		11.3	32	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
15	c2ka2B_	Alignment		11.3	32	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
16	c2ka1B_	Alignment		11.3	32	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
17	c2ka2A_	Alignment		11.3	32	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
18	c2hw2A_	Alignment		9.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rifampin adp-ribosyl transferase; **PDBTitle:** crystal structure of rifampin adp-ribosyl transferase in2 complex with rifampin
19	c2jwaA_	Alignment		9.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
20	c2j5dA_	Alignment		8.6	32	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** nmr structure of bnip3 transmembrane domain in lipid2 bicelles
21	d2d6fc1	Alignment	not modelled	7.6	23	**Fold:**GatB/YqeY motif **Superfamily:**GatB/YqeY motif **Family:**GatB/GatE C-terminal domain-like
22	d1ntca_	Alignment	not modelled	7.2	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
23	d1g2ha_	Alignment	not modelled	6.9	38	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
24	c2b9sB_	Alignment	not modelled	6.3	50	**PDB header:**isomerase/dna **Chain:** B: **PDB Molecule:**dna topoisomerase i-like protein; **PDBTitle:** crystal structure of heterodimeric l. donovani2 topoisomerase i-vanadate-dna complex